

Sequence Listing

RECEIVED

DEC 1 2 2002

TECH CENTER 1600/2900

<110> Adams, Sean Pan, James Zhong, Alan

<120> UCP4

<130> P1626R1

<140> US 09/397,342

<141> 1999-09-15

<150> US 60/101,279

<151> 1998-09-22

<150> US 60/114,223

<151> 1998-12-30

<150> US 60/129,674

<151> 1999-04-16

<160> 18

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<211> 323

<212> PRT

<213> Homo sapiens

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Arg Trp Pro Arg Ala Ser Lys Phe Leu Leu Ser Gly Cys Ala Ala 20 25 30

Thr Val Ala Glu Leu Ala Thr Phe Pro Leu Asp Leu Thr Lys Thr 35 40 45

Arg Leu Gln Met Gln Gly Glu Ala Ala Leu Ala Arg Leu Gly Asp 50 55 60

Gly Ala Arg Glu Ser Ala Pro Tyr Arg Gly Met Val Arg Thr Ala 65 70 75

Leu Gly Ile Ile Glu Glu Gly Phe Leu Lys Leu Trp Gln Gly 80 85 90

Val Thr Pro Ala Ile Tyr Arg His Val Val Tyr Ser Gly Gly Arg
95 100 105

Met Val Thr Tyr Glu His Leu Arg Glu Val Val Phe Gly Lys Ser 110 115 120

Glu Asp Glu His Tyr Pro Leu Trp Lys Ser Val Ile Gly Gly Met 125 130 135

Met Ala Gly Val Ile Gly Gln Phe Leu Ala Asn Pro Thr Asp Leu 140 145 150

Val Lys Val Gln Met Gln Met Glu Gly Lys Arg Lys Leu Glu Gly 155 160 165



Lys Pro Leu Arg Phe Arg Gly Val His His Ala Phe Ala Lys Ile 170 Leu Ala Glu Gly Gly Ile Arg Gly Leu Trp Ala Gly Trp Val Pro 195 185 Asn Ile Gln Arg Ala Ala Leu Val Asn Met Gly Asp Leu Thr Thr Tyr Asp Thr Val Lys His Tyr Leu Val Leu Asn Thr Pro Leu Glu Asp Asn Ile Met Thr His Gly Leu Ser Ser Leu Cys Ser Gly Leu 230 235 240 Val Ala Ser Ile Leu Gly Thr Pro Ala Asp Val Ile Lys Ser Arg 250 245 Ile Met Asn Gln Pro Arg Asp Lys Gln Gly Arg Gly Leu Leu Tyr 270 Lys Ser Ser Thr Asp Cys Leu Ile Gln Ala Val Gln Gly Glu Gly 280 Phe Met Ser Leu Tyr Lys Gly Phe Leu Pro Ser Trp Leu Arg Met 300 290 295 Thr Pro Trp Ser Met Val Phe Trp Leu Thr Tyr Glu Lys Ile Arg Glu Met Ser Gly Val Ser Pro Phe

<210> 2

<211> 1039

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<213> Homo sapiens

320

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gggctttggg caggctggt acccaatata caaagagcag cactggtgaa 650 tatgggagat ttaaccactt atgatacagt gaaacactac ttggtattga 700 atacaccact tgaggacaat atcatgactc acggtttatc aagtttatgt 750 tctggactgg tagcttctat tctgggaaca ccagccgatg tcatcaaaag 800 cagaataatg aatcaaccac gagataaaca aggaagggga cttttgtata 850 aatcatcgac tgactgcttg attcaggctg ttcaaggtga aggattcatg 900 agtetatata aaggettttt accatettgg etgagaatga eeeettggte 950 aatggtgttc tggcttactt atgaaaaaat cagagagatg agtggagtca 1000 gtccatttta agaattctgc agatatccat cacactggc 1039 <210> 3 <211> 31 <212> DNA <213> Artificial <220> <221> Misc-feature <222> 1-31 <223> Sequence is synthesized <400> 3 cgcggatccc gttatcgtct tgcgctactg c 31 <210> 4 <211> 34 <212> DNA <213> Artificial <220> <221> Misc-feature <222> 1-34 <223> reverse primer <400> 4 gcggaattct taaaatggac tgactccact catc 34 <210> 5 <211> 1248 <212> DNA <213> Artificial <220> <221> Misc-feature <222> 1-1248 <223> Sequence is synthesized <220> <221> unsure <222> 1231 <223> unknown base <400> 5 cgttatcgtc ttgcgctact gctgaatgtc cgtcccggag gaggaggaga 50 ggcttttgcc gctgacccag agatggcccc gagcgagcaa attcctactg 100

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 gagacggtgc aagagaatct gccccctata ggggaatggt gcgcacagcc 250
 ctagggatca ttgaagagga aggctttcta aagctttggc aaggagtgac 300
 accegecatt tacagacacg tagttattte tggaggtega atggteacat 350
 atgaacatct ccgagaggtt gtgtttggca aaagtgaaga tgagcattat 400
 cccctttgga aatcagtcat tggagggatg atggctggtg ttattggcca 450
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 cctaaagatg caacccttaa agatacagtg ttcagtatta ttgaaatatg 1050
 ggcatctgca acacataccc cctattattt ctacctcttt aggaagacac 1100
 ctattccaca gagactgatt tatagggggc agcactttat ttttttctgg 1150
 aaacccaagt tetetttgae teetettttt gteeaaaagt gatetggteg 1200
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<211> 58
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<213> Artificial
<220>
<221> Misc-feature
<222> 1-58
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ggaggagg 58
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<210> 7 <211> 35

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  <211> 33
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  <213> Artificial
  <220>
  <221> Misc-feature
  <222> 1-33
  <223> reverse primer
  <400> 8
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  <211> 61
  <212> DNA
  <213> Artificial
 <220>
  <221> Misc-feature
  <222> 1-61
  <223> Sequence is synthesized
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  gccttcagac g 61
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  <211> 19
  <212> DNA
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 <221> Misc-feature
 <222> 1-19
 <223> Sequence is synthesized
 <400> 10
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 <210> 11
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 <222> 1-20
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<223> reverse primer

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 <222> 1-22
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 <210> 13
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 <222> 1-24
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 <210> 14
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 <222> 1-23
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  ctccttctgc atcctgtcag caa 23
 <210> 15
 <211> 22
 <212> DNA
 <213> Artificial
 <220>
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 <222> 1-22
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 <211> 307
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<212> PRT

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Ala Cys Thr Ser Arg Glu Ala Pro Phe 305

260

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265

270

	-	-1	_	_ ,	- 4				-1			-	- 1	- 1	-
	Leu	GLY	Ser	Trp	Asn	Val	Val	Met	Phe	Val	Thr	Tyr	GLu	GIn	
					275				^	280					285
•															
	Lys	Arg	Ala	Leu		_	Val				_	Glu			Phe